

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/735,289  
Source: J Two  
Date Processed by STIC: 71-19-04

# ENTERED



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/735,289

DATE: 11/19/2004

TIME: 17:05:48

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\11192004\J735289.raw

4 <110> APPLICANT: Zhu, J.  
 5       Ding, A.  
 6       Nathan, C.  
 8 <120> TITLE OF INVENTION: Use of proepithelin to promote wound  
 9       repair and reduce inflammation  
 11 <130> FILE REFERENCE: 1676.011US1  
 13 <140> CURRENT APPLICATION NUMBER: US 10/735,289  
 14 <141> CURRENT FILING DATE: 2003-12-12  
 16 <150> PRIOR APPLICATION NUMBER: 60/432,948  
 17 <151> PRIOR FILING DATE: 2002-12-12  
 19 <160> NUMBER OF SEQ ID NOS: 32  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 593  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Homo sapiens  
 28 <400> SEQUENCE: 1  
 29 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala  
 30     1               5               10               15  
 31 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu  
 32     20              25              30  
 33 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys  
 34     35              40              45  
 35 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp  
 36     50              55              60  
 37 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr  
 38     65              70              75              80  
 39 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His  
 40     85              90              95  
 41 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys  
 42     100             105             110  
 43 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp  
 44     115             120             125  
 45 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp  
 46     130             135             140  
 47 Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp  
 48     145             150             155             160  
 49 Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr  
 50     165             170             175  
 51 Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro  
 52     180             185             190  
 53 Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Val Met Cys  
 54     195             200             205

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55 Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu  
 56 210 215 220  
 57 Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys  
 58 225 230 235 240  
 59 Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile  
 60 245 250 255  
 61 Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr  
 62 260 265 270  
 63 Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val  
 64 275 280 285  
 65 Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp  
 66 290 295 300  
 67 Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His  
 68 305 310 315 320  
 69 Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu  
 70 325 330 335  
 71 Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu  
 72 340 345 350  
 73 Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn  
 74 355 360 365  
 75 Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly  
 76 370 375 380  
 77 Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His  
 78 385 390 395 400  
 79 Gln His Cys Cys Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys  
 80 405 410 415  
 81 Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg  
 82 420 425 430  
 83 Arg Ala Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr  
 84 435 440 445  
 85 Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp  
 86 450 455 460  
 87 Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His  
 88 465 470 475 480  
 89 Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu  
 90 485 490 495  
 91 Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro  
 92 500 505 510  
 93 His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His  
 94 515 520 525  
 95 Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys  
 96 530 535 540  
 97 Pro Tyr Arg Gln Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro  
 98 545 550 555 560  
 99 Ala Gly Phe Arg Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu  
 100 565 570 575  
 101 Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu  
 102 580 585 590  
 103 Leu

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Input Set : A:\Sequence Listing.txt

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107 <210> SEQ ID NO: 2  
 108 <211> LENGTH: 593  
 109 <212> TYPE: PRT  
 110 <213> ORGANISM: Homo sapiens  
 112 <400> SEQUENCE: 2  
 113 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala  
 114 1 5 10 15  
 115 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu  
 116 20 25 30  
 117 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys  
 118 35 40 45  
 119 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp  
 120 50 55 60  
 121 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr  
 122 65 70 75 80  
 123 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His  
 124 85 90 95  
 125 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys  
 126 100 105 110  
 127 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp  
 128 115 120 125  
 129 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp  
 130 130 135 140  
 131 Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp  
 132 145 150 155 160  
 133 Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr  
 134 165 170 175  
 135 Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro  
 136 180 185 190  
 137 Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Val Met Cys  
 138 195 200 205  
 139 Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu  
 140 210 215 220  
 141 Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys  
 142 225 230 235 240  
 143 Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile  
 144 245 250 255  
 145 Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr  
 146 260 265 270  
 147 Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val  
 148 275 280 285  
 149 Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp  
 150 290 295 300  
 151 Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His  
 152 305 310 315 320  
 153 Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu  
 154 325 330 335  
 155 Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu  
 156 340 345 350

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157 Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn  
158 355 360 365  
159 Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly  
160 370 375 380  
161 Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His  
162 385 390 395 400  
163 Gln His Cys Cys Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys  
164 405 410 415  
165 Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg  
166 420 425 430  
167 Arg Ala Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr  
168 435 440 445  
169 Ser Cys Pro Val Gly Gln Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp  
170 450 455 460  
171 Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His  
172 465 470 475 480  
173 Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu  
174 485 490 495  
175 Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro  
176 500 505 510  
177 His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His  
178 515 520 525  
179 Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys  
180 530 535 540  
181 Pro Tyr Arg Gln Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro  
182 545 550 555 560  
183 Ala Gly Phe Arg Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu  
184 565 570 575  
185 Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu  
186 580 585 590  
187 Leu  
191 <210> SEQ ID NO: 3  
192 <211> LENGTH: 2178  
193 <212> TYPE: DNA  
194 <213> ORGANISM: Homo sapiens  
196 <400> SEQUENCE: 3  
197 gtagtctgag cgctaccgg ttgctgtgc ccaaggacccg cggagtcgga cgcaaggcaga 60  
198 ccatgtggac cctggtgagc tgggtggcct taacagcagg gctggtggt ggaacgcgg 120  
199 gcccagatgg tcagttctgc cctgtggcct gctgcctgga ccccgagggaa gccagctaca 180  
200 gctgctgcgg tccccctctg gacaaatggc ccacaaact gaggcaggcat ctgggtggcc 240  
201 cctgccagg ttagtccccac tgctctgcgg gccactctg catcttacc gtctcaggga 300  
202 cttccaggta ctgcccccttc ccagaggccg tggcatgcgg ggatggccat cactgctgcc 360  
203 cacggggctt ccactgcagt gcagacgggc gatctgcctt ccaaagatca ggtacaact 420  
204 ccgtgggtgc catccaggta cctgatagtc agttcaatg cccggacttc tccacgtgt 480  
205 gtgttatgtt cgatggctcc tgggggtgtt gccccatgcgc ccaggcttcc tgctgtgaag 540  
206 acagggtgca ctgctgtccg cacggtgccct tctgcgaccc ggttcacacc cgctgcata 600  
207 cacccacggg caccaccccc ctggcaaaga agctcccgtc ccagaggact aacagggcag 660  
208 tggccttgtc cagctcggtc atgtgtccgg acgcacggtc ccgggtccct gatggttcta 720  
209 octgctgtga gctgcccagt gggaaagtatg gctgctgccc aatgcccacac gcccacgtgt 780

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210 gctccgatca cctgcactgc tgcccccaag acactgtgtg tgacctgatc cagagtaagt 840  
211 gcctctccaa ggagaacgc accacggacc tcctcaactaa gtcgcctgcg cacacagtgg 900  
212 gggatgtgaa atgtgacatcg gaggtgagct gcccagatgg ctataacctgc tgccgtctac 960  
213 agtccccggc ctggggctgc tgccctttt cccaggtgt gtgctgttag gaccacatac 1020  
214 actgtgtgcc cgccccgttt acgtgtgaca cgcagaaggg tacctgtgaa cagggccccc 1080  
215 accaggtgcc ctggatggag aaggccccag ctcacccat cctgcccagac ccacaagcct 1140  
216 tgaagagaga tgtccccctgt gataatgtca gcagctgtcc ctccctccgat acctgctgcc 1200  
217 aactcacgtc tggggagtgg ggctgtgtc caatcccaga ggctgtctgc tgctcgacc 1260  
218 accagcactg ctgccccccag ggctacacgt gtgtagctga ggggcagtgt cagcgagggaa 1320  
219 gcgagatcgt ggctggactg gagaagatgc ctgcccccccg ggcttcctta tcccaaaaaa 1380  
220 gagacatcgg ctgtgaccag cacaccagct gcccqgtqgg gcagacactgc tgcccgagcc 1440  
221 tgggtgggag ctgggcctgc tgccagttgc cccatgtgt gtgctgcggag gatcgccagc 1500  
222 actgtgtgcc ggctggctac acctgcaacg tgaaggctcg atcctgcggag aaggaagtgg 1560  
223 tctctgcccc gcctgcacc ttccctggccc gtgcctca cgtgggtgtg aaggacgtgg 1620  
224 agtgtgggaa aggacacttc tgccatgata accagacctg ctgcccggagac aaccgacagg 1680  
225 gctgggcctg ctgtccctac cggcaggcgct tctgttgtgc tgatcgccgc cactgctgtc 1740  
226 ctgctggctt cgcgtgcgc gccagggtt ccääagtgttt ggcgcaggggag gccccgcgtc 1800  
227 gggacgcccc ttgaggggac ccagccttga gacagctgt gtgaggggaca gtactgaaga 1860  
228 ctctgcagcc ctggggaccc cactcgagggtg tgccctctg ctcaggcctc cctagcacct 1920  
229 ccccttaacc aaattctccc tgaccccat tctgagctcc ccatcaccat gggaggtggg 1980  
230 gcctcaatct aaggccttcc ctgtcagaag ggggttgtgg caaaagccac attacaagct 2040  
231 gccatccccct ccccgttca gtggaccctg tggccaggtg ctttcccta tccacagggg 2100  
232 tgggtgtgtg tggcgcgtg tgcgtttcaa taaagttgt acacttcaa aaaaaaaaaaa 2160  
233 aaaaaaaaaaa aaaaaaaaaa 2178

236 <210> SEQ ID NO: 4

237 <211> LENGTH: 589

238 <212> TYPE: PRT

239 <213> ORGANISM: M

241 <400> SEQUENCE: 4  
 242 Met Trp Val Leu Met Ser Trp Leu Ala Phe Ala Ala Gly Leu Val Ala  
 243 1 5 10 15  
 244 Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu  
 245 . 20 25 30  
 246 Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys Asn Pro Leu Leu Asp Thr  
 247 35 40 45  
 248 Trp Pro Arg Ile Thr Ser His His Leu Asp Gly Ser Cys Gln Thr His  
 249 50 55 60  
 250 Gly His Cys Pro Ala Gly Tyr Ser Cys Leu Leu Thr Val Ser Gly Thr  
 251 65 70 75 80  
 252 Ser Ser Cys Cys Pro Phe Ser Lys Gly Val Ser Cys Gly Asp Gly Tyr  
 253 85 90 95  
 254 His Cys Cys Pro Gln Gly Phe His Cys Ser Ala Asp Gly Lys Ser Cys  
 255 100 105 110  
 256 Phe Gln Met Ser Asp Asn Pro Leu Gly Ala Val Gln Cys Pro Gly Ser  
 257 115 120 125  
 258 Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys Cys Ile Met Val Asp Gly  
 259 130 135 140  
 260 Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg  
 261 145 150 155 160

VERIFICATION SUMMARY  
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